

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/565,646
Source: IFWP
Date Processed by STIC: 1/30/06

ENTERED

CRF Errors Edited by the STIC Systems Branch

Serial Number: 10/565,646

CRF Edit Date: 2/2/06
Edited by: M

— Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

— Corrected the SEQ ID NO. Sequence numbers edited were:

— Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

— Deleted: _____ invalid beginning/end-of-file text ; _____ page numbers

— Inserted mandatory headings/numeric identifiers, specifically:

— Moved responses to same line as heading/numeric identifier, specifically:

— Other:
Inserted amino acid numbers in sequences 1,3,5



IFWP

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/565,646

DATE: 02/02/2006
TIME: 18:12:35

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF4\02022006\J565646.raw

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3 <110> APPLICANT: INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE
5 <120> TITLE OF INVENTION: USE OF THE SILVER GENE FOR THE AUTHENTIFICATION OF
6   THE ORIGINAL BREED OF ANIMAL POPULATIONS AND
7   THEIR DERIVATIVE PRODUCTS
9 <130> FILE REFERENCE: IFB 03 BT INR SILV
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/565,646
C--> 11 <141> CURRENT FILING DATE: 2006-01-24
11 <160> NUMBER OF SEQ ID NOS: 11
13 <170> SOFTWARE: PatentIn version 3.1
15 <210> SEQ ID NO: 1
16 <211> LENGTH: 8146
17 <212> TYPE: DNA
18 <213> ORGANISM: Bos taurus
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22 <222> LOCATION: (30)..(105)
23 <223> OTHER INFORMATION:
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27 <222> LOCATION: (2326)..(2436)
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53 <223> OTHER INFORMATION:
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56 <221> NAME/KEY: CDS

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Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF4\02022006\J565646.raw

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 58 <223> OTHER INFORMATION:
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 61 <221> NAME/KEY: CDS
 62 <222> LOCATION: (6875)..(7080)
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 73 <223> OTHER INFORMATION:
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 77 Met Asp Leu Val Leu Arg Lys Tyr
 78 1 5
 80 ctt ctc cat gtg gct ctg atg ggt gtt ctt ctg gct gta ggg acc aca 101
 81 Leu Leu His Val Ala Leu Met Gly Val Leu Leu Ala Val Gly Thr Thr
 82 10 15 20
 84 gaa g gtgagtgtgg gatgttgac atgaacaagt gtgaatttgg gttgcacac 155
 85 Glu
 86 25
 88 ctgctctggc tttctctcc ctaaatggc agatatcagt agtgcttcag gtgtctccc 215
 89 cccatttgc tttagtgagga catggcaac tgagctccct ccccacatga agatttgggt 275
 90 gcatgtgtgt tcaggcactt gggactgaac ctgaaaacaa ccccatctac ctggatgggt 335
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 92 atgggtgccaa aggttagaaa atgagtggaa actcatttag gcttgcctc aggcaactgg 455
 93 gataagggtat tttaggagata gagaaagata ggagatagga gaaaggagaa agaggatgtg 515
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 95 acagcccagg cttttttctt gggctggaa gagacaggca gaagggtctc agctgagcat 635
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 107 ccaaaaaaaca aacgaacaac aaaaataaaag gatagataaa gcaaatgtga caaaatgtgc 1355
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113	cccccaactct	atcttcttgg	cctcatctct	catgatgtac	atcagccaca	ttgctagtgt	1715										
114	ctgctcatgg	ccttctgcct	agaatgc tt	atgccccagc	caactattta	ctgtcttctt	1775										
115	cagtcgacca	gagtgaatt	tacctgttta	aaatctatca	ttttgttata	cattgtgcat	1835										
116	gtctattatg	gctcatatta	agcaatgc ct	tggattatag	taatttatgt	atatgtctat	1895										
117	ttcatatact	ttaacctgaa	ccc cttcaga	accatttctt	tttcat tttctt	taagttcttt	1955										
118	gcacctagcc	cagtgcctgg	tacgtcg tgg	gtattcagta	gattaaaatg	cactttaagg	2015										
119	aacttccctt	gttgc cc atc	aagtggctaa	ggctctgtgc	tcccaatgca	ggggaccagg	2075										
120	gttcaatctc	aggtcaggga	actagatccc	acagg tcaca	actaagagtt	tgcaagccac	2135										
121	aactacctg a	cctc acatgc	cacaactaa	cgaagatccc	tcgtgctgca	actaagtcc	2195										
122	agtgc agtta	aatatatttt	ttaatgcac	tttgaatgtg	agaatgaatg	atgtgtcaca	2255										
123	gacactgtt g	tccc ctgaga	agggagtgag	taatgattt g	agggccctca	tagtatatct	2315										
125	tccttttag	ga	ccc aga gac	agg gac tgg	ctt ggt gtc	tca agg cag	2363										
126	Gly	Pro	Arg	Asp	Arg	Trp	Leu	Gly	Val	Ser	Arg	Gln					
127		30		35													
129	ctc	aga	att	aaa	gca	tgg	aac	aga	cag	ctg	tat	cca	gag	tgg	aca	gaa	2411
130	Leu	Arg	Ile	Lys	Ala	Trp	Asn	Arg	Gln	Leu	Tyr	Pro	Glu	Trp	Thr	Glu	
131	40		45		50												
133	agc	cag	ggg	cct	gac	tgc	tgg	aga	g	gtaggaactt	ggcaatttcc	2456					
134	Ser	Gln	Gly	Pro	Asp	Cys	Trp	Arg									
135	55		60														
137	aggaggata	tgg tggaaat	gggtggggag	gggaacgggg	ttgaatgtac	tttaggaagat	2516										
138	aggaaggaa	aaggcataca	gggaggagaa	gccaggagc	taattaatgc	agctgccctt	2576										
140	ttcag	gt	ggc	cac	ata	tcc	ctg	aag	gtc	agc	aat	gat	ggg	cct	aca	ctg	2625
141	Gly	Gly	His	Ile	Ser	Leu	Lys	Val	Ser	Asn	Asp	Gly	Pro	Thr	Leu		
142	65		70		75												
144	att	ggg	gca	aat	gct	tcc	tcc	tat	gcc	ttg	cac	ttt	cct	aaa	agc	2673	
145	Ile	Gly	Ala	Asn	Ala	Ser	Phe	Ser	Ile	Ala	Leu	His	Phe	Pro	Lys	Ser	
146	80		85		90												
148	caa	aag	gtg	ctg	cca	gat	ggg	cag	gtc	atc	tgg	gcc	aac	aac	acc	atc	2721
149	Gln	Lys	Val	Leu	Pro	Asp	Gly	Gln	Val	Ile	Trp	Ala	Asn	Asn	Thr	Ile	
150	95		100		105												
152	atc	aat	g	gtgagta cct	ctccgcctcc	ttcccaaggt	ccagaatccc	ttgtatcccc	2778								
153	Ile	Asn															
154	110																
156	aatgagctca	aggaatcctc	ctcctcttt	ttttttttt	tttttacaaa	ttatatatgt	2838										
157	aacacatatt	cactgc gaa	aaat tagaaa	acacagataa	acaaaaaaga	aaaaaaaatta	2898										
158	tagtccccca	aatggggcac	agaagacca	gtggacatag	aagttggata	gacttggatt	2958										
159	taaactgggt	accat tagt	gaccctggac	aagtca ctga	attgtttgt	tcttccattc	3018										
160	ccttatctat	agaatgggga	tgataacact	ttaaaagggt	ctt gtaagga	ttaaaatgtg	3078										
161	ataatataata	aagat tttag	cataatgc ct	gccctgtgct	gtgcttagta	ccttagttt a	3138										
162	gacgcttgc	aacccatgg	actgtg tagccc	accaggctcc	tctgtccatg	ttgattctgc	3198										
163	aggcaagaat	actggagtg	gtc accatgc	actc ctccag	gggatctcc	caactcagg	3258										
164	atcgaaccca	ggtcctagcc	tacatgttta	attgatgtc	ttat ttttac	ttttatccca	3318										
165	ctagctagag	cacatcatcc	tagacattt	gatacatggc	ctaccaattt	gtgtccagtg	3378										
166	taagaatata	catgtgtgt	ctc agtgg	cagt cgtgtc	tgactt tttg	caacccatg	3438										
167	gactgt tagcc	cgc gaaagct	cctctgc cca	tg ggattg	cc	cagccaa gaa	tactggagca	3498									
168	ggttgc catt	tctt cctcca	ggggatctt	caacacagg	attgaatct	tgtc tctgt	3558										
169	gtt cctgca	ttggcagg	tg tatttttac	cactg agc	ccttggaaac	cccttaagta	3618										
170	tatacacata	aatctttat	agtttccatt	ctcccttcta	ccactccaaa	tagttata	3678										

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Input Set : A:\PTO.AMC.txt

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171	caaggagaat	gtatttttgtt	agctaggcag	tattcctgga	gcccccctct	gggagtcatg	3738
172	ttaaagggtt	tggtgtacag	tgaggaatgc	caggattga	gggagacttg	ctgtcttctt	3798
174	ttcag gg	agc cag	gtg tgg	gga gga	cag ctg	gtat ccc caa	3847
175	Gly Ser Gln Val Trp	Gly Gly Gln	Leu Val Tyr Pro	Gln Glu Pro			
176	115		120		125		
178	gat gat acc	tgc atc ttc	ccc gat	ggg gag	ccc tgc	cct tct ggc cct	3895
179	Asp Asp Thr Cys	Ile Phe Pro Asp	Gly Glu Pro	Cys Pro Ser	Gly Pro		
180	130		135		140		
184	cta tct cag	aaa aga tgc	ttt gtt	tat gtc	tgg aag	acc tgg g	3938
185	Leu Ser Gln Lys	Arg Cys Phe	Val Tyr Val Trp	Lys Thr Trp			
186	145		150		155		
188	gtaagaggtt	cccttctctg	gcctgtcatt	cacactaaa	ttcacttctt	cctacacctat	3998
189	cccccttctt	ttggctctcat	ccttaaatc	tgtgagttc	cctaatttc	acttccccc	4058
190	tgactccttc	ctcttccaca	gcaccttagtc	aactctatta	tacttcttc	tgggagccct	4118
191	gctccaatta	tagtccatc	ccatggaccc	tctcataagg	actttttcc	tgcacaaat	4178
192	atgcaagctt	aaactctctg	aaataaccat	ccttgataca	tctcctgacc	ttccttctct	4238
193	ggttccatct	ctaaccctgc	cccagtctcc	tttgaccagt	aaccccttc	cctactcttc	4298
195	tttccaaaaaa	cctcag ac	caa tac tgg	caa gtt ctg	ggg ggc	cca gtg tct	4349
196							
197							
199	gga ctg agc	atc ggg aca	gac aag	gca atg	ctg ggc	aca tat aac	4397
200	Gly Leu Ser Ile	Gly Thr Asp	Lys Ala Met	Leu Gly Thr	Tyr Asn	Met	
201	170		175		180		
203	gaa gtg act	gtc tac cac	cac cgc	cgg ggg	tcc cag	agc tat	4445
204	Glu Val Thr Val	Tyr His Arg	Arg Gly Ser	Gln Ser Tyr	Val Pro	Leu	
205	185		190		195		200
207	gct cac tcc	agt tca gcc	ttc acc att	act g	gtaaggactg	aggagggac	4496
208	Ala His Ser Ser	Ala Phe Thr	Ile Thr				
209	205		210				
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212	ggaaatggtg	tgtaacctta	cagggcaga	accaggaaga	tgtggcaga	ggatgtggg	4616
213	gcttggagcc	cgtgaagggc	caggcagctt	gggttgggtt	aaaaatatgg	ctgtgaaaga	4676
215	agaagctgac	agaaagaaga	acttatggtt	ctcacttct	ctgactccaa	tcccg ac	4734
216						Asp	
219	cag gtg ccc	ttc tct	gtg agt	gtg tct	cag ctg	cag gcc ttg	4782
220	Gln Val Pro	Phe Ser Val	Ser Val	Ser Gln	Leu Gln	Ala Leu Asp	Gly
221	215		220		225		
223	agg aac aag	cgc ttc	ctg aga	aag cag	cct ctg	acc ttt gcc ctc	4830
224	Arg Asn Lys	Arg Phe	Leu Arg	Lys Gln	Pro Leu	Thr Phe	Ala Leu Gln
225	230		235		240		
227	ctc cat	gat ccc	agt ggc	tat ttg	gct ggg	gct gac ctt tcc	4878
228	Leu His Asp	Pro Ser Gly	Tyr Leu Ala	Gly Ala	Asp Leu	Ser Tyr	Thr
229	245		250		255		
231	tgg gac ttt	ggt gac	agt aca	ggg acc	ctg atc	tct cgg gca	4926
232	Trp Asp Phe	Gly Asp Ser	Thr Gly	Thr Leu	Ile Ser	Arg Ala	Leu Thr
233	260		265		270		275
235	gtc act cac	act tac	cta gag	tct ggc	cca gtc	act gca	4974
236	Val Thr His	Thr Tyr Leu	Glu Ser Gly	Pro Val	Thr Ala	Gln Val	Val
237	280		285		290		

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241					295				300							305		
245	ggc	act	aca	gat	agg	cat	gtg	aca	act	gca	gag	gct	cct	gga	acc	aca		5070
246	Gly	Thr	Thr	Asp	Arg	His	Val	Thr	Thr	Ala	Glu	Ala	Pro	Gly	Thr	Thr		
247									310							320		
249	gct	ggc	caa	gtg	cct	act	aca	gaa	gtc	atg	ggc	acc	aca	cct	ggc	cag		5118
250	Ala	Gly	Gln	Val	Pro	Thr	Thr	Glu	Val	Met	Gly	Thr	Thr	Pro	Gly	Gln		
251									325							335		
253	gtg	cca	act	gca	gag	gcc	cct	ggc	acc	aca	gtt	ggg	tgg	gtg	cca	acc		5166
254	Val	Pro	Thr	Ala	Glu	Ala	Pro	Gly	Thr	Thr	Val	Gly	Trp	Val	Pro	Thr		
255							340				345					350		355
257	aca	gag	gat	gta	ggt	acc	aca	cct	gag	cag	gtg	gca	acc	tcc	aaa	gtc		5214
258	Thr	Glu	Asp	Val	Gly	Thr	Thr	Pro	Glu	Gln	Val	Ala	Thr	Ser	Lys	Val		
259									360			365				370		
261	tta	agt	aca	aca	cca	gtg	gag	atg	cca	act	gca	aaa	gct	aca	ggt	agg		5262
262	Leu	Ser	Thr	Thr	Pro	Val	Glu	Met	Pro	Thr	Ala	Lys	Ala	Thr	Gly	Arg		
263							375				380					385		
265	aca	cct	gaa	gtg	tca	act	aca	gag	ccc	tct	gga	acc	aca	gtt	aca	cag		5310
266	Thr	Pro	Glu	Val	Ser	Thr	Glu	Pro	Ser	Gly	Thr	Thr	Val	Thr	Gln			
267									390			395				400		
269	gga	aca	act	cca	gag	ctg	gtg	gag	acc	aca	gct	gga	gag	gtg	tcc	act		5358
270	Gly	Thr	Thr	Pro	Glu	Leu	Val	Glu	Thr	Thr	Ala	Gly	Glu	Val	Ser	Thr		
271								405			410				415			
273	cct	gag	cct	gct	ggt	tca	aat	act	agc	tca	ttc	atg	cct	aca	gaa	ggt		5406
274	Pro	Glu	Pro	Ala	Gly	Ser	Asn	Thr	Ser	Ser	Phe	Met	Pro	Thr	Glu	Gly		
275							420			425			430			435		
277	act	gca	g	gtaa	ggggc	caccat	gaat	gat	ttc	atag	agg	tttggggca	tttgcacag					5463
278	Thr	Ala																
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282	tgg	at	cccc	tc	aga	at	c	t	c	ttt	gg	cc	cc	ttt	cc	ttt	cc	5583
283	aat	at	agat	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	5643
284	tct	c	t	t	t	c	t	t	c	t	t	c	t	t	c	t	5703	
285	tca	tgt	c	t	t	t	c	t	t	c	t	t	c	t	t	c	5763	
286	ttt	cc	c	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	5823	
287	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	5883	
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292	ttt	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	6183	
293	ttt	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	6243	
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296	ttt	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	6352	
297	tta	at	cct	c	c	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	
298																		
300	acc	tta	gtc	ctg	gag	aag	cgc	caa	gcc	ccc	ctg	gat	tgt	gtt	ctg	tat		6400
301	Thr	Leu	Val	Leu	Glu	Lys	Arg	Gln	Ala	Pro	Leu	Asp	Cys	Val	Leu	Tyr		
302									450						455			

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 02/02/2006
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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:3; Line(s) 823
Seq#:5; Line(s) 1224

VERIFICATION SUMMARY

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Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\02022006\J565646.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:30 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:23
L:35 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:28
L:40 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:33
L:45 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:38
L:50 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:43
L:55 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:48
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L:75 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:68
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L:535 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:528
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L:699 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 3
L:1036 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:1028
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Raw Sequence Listing before editing (for reference only)



IFWP

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/565,646

DATE: 01/30/2006
TIME: 16:00:01

Input Set : A:\PTO.SS.txt
Output Set: N:\CRF4\01302006\J565646.raw

3 <110> APPLICANT: INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE
5 <120> TITLE OF INVENTION: USE OF THE SILVER GENE FOR THE AUTHENTIFICATION OF
6 THE ORIGINAL BREED OF ANIMAL POPULATIONS AND
7 THEIR DERIVATIVE PRODUCTS
9 <130> FILE REFERENCE: IFB 03 BT INR SILV
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/565,646
C--> 11 <141> CURRENT FILING DATE: 2006-01-24
11 <160> NUMBER OF SEQ ID NOS: 11
13 <170> SOFTWARE: PatentIn version 3.1

ERRORED SEQUENCES

1587 <210> SEQ ID NO: 11
1588 <211> LENGTH: 30
1589 <212> TYPE: DNA
1590 <213> ORGANISM: Artificial sequence
1592 <220> FEATURE:
1593 <223> OTHER INFORMATION: Primer
1595 <400> SEQUENCE: 11
1596 cagtcccaag tgcctgaaca cacatgcacc
E--> 1605 (1) *delete*

*Does Not Comply
Corrected Diskette Needed*

see pp 1-5

30

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from sequence 1

atttccagg caagaacact ggagtgggtg gccatttcct tctccagggg atttccctg	5823
cccaggatt aaacccgaat tggcagggtgg attcttacc cgagccaccc agaaagtccc	5883
atgtgatcat tagataatac ttatcacca ttttctgatt aagtgtaaac acagaaatct	5943
ttctgacacc acttcccacc cctggattcc catcccaaag taggttacc tggaattgtg	6003
gttagaatac taaaaaggga gaagtgagat agtgacacta tgacttaaca catgtcaa	6063
gtctgaccca ggacctggca cagtgttaggg tgtgataaac atttgggatg tctaaaattc	6123
tgactctaac cctgtgactc tggggcagtc atttcttgc ggccttctt tatctaaaa	6183
aatgagagtt tccagcttt gtctgattct aagcctggat ccagtagctc tgactctacc	6243
tggaaaaatg ctgttgggc ctgtttcag gttagtcatt tgcttttgc cttgcctct	6303
ttaatcctct cctccag gc tcc ctg agt ccc ctg ccg gat gac act gcc	6352
Gly Ser Leu Ser Pro Leu Pro Asp Asp Thr Ala	
440	445
acc tta gtc ctg gag aag cgc caa gcc ccc ctg gat tgt gtt ctg tat	6400
Thr Leu Val Leu Glu Lys Arg Gln Ala Pro Leu Asp Cys Val Leu Tyr	
450	455
460	
cgc tat ggc tcc ttt tcc ctc acc ctg gac att gtc c gtgagtcttg	6447
Arg Tyr Gly Ser Phe Ser Leu Thr Leu Asp Ile Val	
465	470
475	
cctacattgt ccgttaagctg gtggagggag gcgtgtgctg cttagggttg cccagtggaa	6507
gcacaccttg gaaggaatta ctcacctgga caaggagaat acccagatcc caggggttcc	6567
atatgaaggc agaatggat tagggaggca gcccaggac cttcctggcc atgggccttg	6627
ggggaggata agtagaggag tctcagactt aaaaaaatct tgcaactttg cag ag	6682
Gln	
ggt att gag agt gct gag atc cta cag gct gtg tca tcc agt gaa gga	6730
Gly Ile Glu Ser Ala Glu Ile Leu Gln Ala Val Ser Ser Glu Gly	
480	485
490	
gat gca ttt gag ctg act gtg tct tgc caa ggc gg gtgagtgtcc	6775
Asp Ala Phe Glu Leu Thr Val Ser Cys Gln Gly Gly	
495	500
<i>SOSL-Insert</i>	
cacgggtgcc ctgagaactc ctggggtgac tgctgtcctg ttctctgggtg tctagtgtcc	6835
cttcccgat tccctgacgt aagctgacat ctctcccgag g cta ccc aag gaa gcc	6890
Leu Pro Lys Glu Ala	
510	
tgc atg gac atc tca tcg cca ggg tgt cag ctg cct gcc cag cgg ctg	6938
Cys Met Asp Ile Ser Ser Pro Gly Cys Gln Leu Pro Ala Gln Arg Leu	
515	520
525	
tgt cag cct gtg ccc ccc agc cca gcc tgc cag ctg gtt ttg cac cag	6986
Cys Gln Pro Val Pro Pro Ser Pro Ala Cys Gln Leu Val Leu His Gln	
530	535
540	
gta ctg aag ggt ggc tca ggg acc tac tgc ctc aat gtg tct ttg gct	7034
Val Leu Lys Gly Gly Ser Gly Thr Tyr Cys Leu Asn Val Ser Leu Ala	
545	550
555	

from sequence 3 10/86 S, 646 3

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460	460	
cgc tat ggc tcc ttt tcc ctc acc ctg gac att gtc c gtgagtcttg Arg Tyr Gly Ser Phe Ser Leu Thr Leu Asp Ile Val	465 470	6447
475		
cctacattgt ccgttaagctg gtggagggag gcgtgtctg cttagggttg cccagtggaa gcacaccttgaaggaatta ctcaccttggca caaggagaat acccagatcc caggggtttc atatgaaggc agaatggat tagggaggca gcccaggac cttcctggcc atgggccttg		6507 6567 6627
ggggaggata agtagaggag tctcagactt aaaaaaatct tgcaactttg cag ag Gln	6682	
480	485	
490		
ggt att gag agt gct gag atc cta cag gct gtg tca tcc agt gaa gga Gly Ile Glu Ser Ala Glu Ile Leu Gln Ala Val Ser Ser Ser Glu Gly	480 485	6730
495	500	
500		<i>SOS Insert</i>
cacgggtgcc ctgagaactc ctggggtgac tgctgtcctg ttctctggtg tctagtgtcc		6835
cttccccat tccctgacgt aagctgacat ctctccca g cta ccc aag gaa gcc Leu Pro Lys Glu Ala	510	6890
515		
520		
tgc atg gac atc tca tcg cca ggg tgt cag ctg cct gcc cag cggtctg Cys Met Asp Ile Ser Ser Pro Gly Cys Gln Leu Pro Ala Gln Arg Leu	515 520	6938
525		
tgt cag cct gtg ccc ccc agc cca gcc tgc cag ctg gtt ttg cac cag Cys Gln Pro Val Pro Pro Ser Pro Ala Cys Gln Leu Val Leu His Gln	530 535	6986
540		
gta ctg aag ggt ggc tca ggg acc tac tgc ctc aat gtg tct ttg gct Val Leu Lys Gly Ser Gly Thr Tyr Cys Leu Asn Val Ser Leu Ala	545 550	7034
555		
gat gcc aat agc ctg gcg atg gtc agc acc cag ctt gtc atg cct g Asp Ala Asn Ser Leu Ala Met Val Ser Thr Gln Leu Val Met Pro	560 565	7080
570		
gtaggtagtt ggacaagagg taggatgaag acacggggag atggtagagg ttacctacta		7140
gaggaagcag acactgaatg cagccgtatc tggattcca cccatag gg caa gaa Gly Gln Glu	575	7195
575		
gca ggc ctc agg cag gct cct ctg ttc gtg ggc atc ttg ctg gtg cta		7243

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from Sequence 5

1

5

ctt ctc cat gtg gct ctg atg ggt gtt ctg gct gta ggg acc aca gaa g	102
Leu Leu His Val Ala Leu Met Gly Val Leu Ala Val Gly Thr Thr Glu	
10 15 20	

gtgagtgtgg gatgttggac atgaacaagt gtgaattgg ggttgcacac ctgctctgg	162
ttttctctcc ctaaaaatgga agatatacg tgcgttcag gtgtctccca cccatttgat	222
ttagtgagga catgggcaac tgagctccct ccccacatga agatttgggt gcatgtgtgt	282
tcaggcactt gggactgaac ctgaaaacaa ccccacatcac ctggatgggt gagagaacag	342
tatgtctccg tggccctaattttgagatgc tctgaatagt gagctggAAC atgggtgccA	402
aggttagtaaa atgagtggAA actcatttgc gctttgtctc aggcaattgg gatagggtat	462
ttaggagata gagaagata ggagatagGA gaaaggagAA agaggatgtg gtattggata	522
gaagggtaat gaggcacCTC atccccCTT tgggatgggc atgggtgaAC acagcccagg	582
cttttgtct ggggctggAA gagacaggCA gaagggtctc agctgagcat cacatgaaAG	642
ggctctgggg gattggggcc tcgtgacagg agcaaggcgg gtgggggtgg gatgggtgaga	702
gggtctggAA tggccCGTC tgctctgagg agggaggatt gggagtggaAG aaagaatggg	762
gcatcttATG attctcttGT tcttgtggT aggtattcag tggataattt ctagatcTC	822
ccccaaAGA atcaaccagg ttctctggTA atgttagAGA tgagtgagg atagtctgtg	882
atgtgcAGAA atatctacat tgcACCCAG tgcCcCCTT ctctagatCC ctgggtctCAC	942
agacttcttG gaacttctcc ttgatctgac ttccctcatt catgggtgtCA tttcaagtCT	1002
tattttttA ctatgttCGT tattgtattC tggaaatATC ctgttcatAT gtgtccACCC	1062
aaggctcttA atatgttGTG cttaactttt ggatccAGAT tttaaaATC ataagaAGAC	1122
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attaacattG tgtttatttA agaaaaaaaA atatTTTT acagaaACCT actgaattTG	1242
tagggttttA aaataacatG atgtctggGA tttgcttttG aatgcttCAg ccaaaaaACA	1302
aacgaacaAC aaaaataAAAG gatagataAA gcaaATGTGA caaaatgtCTG atagttgttG	1362
gaccttgggg agacacatGC agagccatCA catcaCTTT tttcagacat CTTTCTTGGT	1422
cagtataatCattttgttGtcccccactC ccaatttCTA ctgcctctA gtccatCCTC	1482
ctcaCTGCTT GccAAAGTGA tccttctAAA acacaAAATCT gatcatATTc AAAAAGCTT	1542
tgaagggtAA gttttatGt atatGCCATA tacagtACA acAAACAAAAA tcgtctgagg	1602
tgcgttGCC tacaggataAA agtccAAACT ctttgcCTG gcaACTCCAGG CCCCCACTCT	1662
atcttcttgg CCTCATCTC catgatgtAC atcagccACA ttgcttagtGT ctgcTCatGG	1722
ccttctgcCT agaatgtCTT atgccccAGC caactattTA ctgtcttCTT cagtcACCA	1782
gagtgcatt tacctgttA aaatctatCA ttttgttATA cattgtgcat gtctattATG	1842
gctcatatta agcaatgcCT tggattatAG taatttATG atatgtCTAT ttcatataCT	1902
ttaacctgAA ccccttcAGA accatttCTT tticatttCT taagttCTT gcacctAGCC	1962
cagtgcctgg tacgtcgtgg gtattcAGTA gattAAATG cactttaAGG aacttccCTT	2022
gttgtccATC aagtggctAA ggctctgtGC tcccaATGCA ggggaccAGG gttcaatCTC	2082
aggtcaggGA actagatCCC acaggTCACA actaAGAGTT tgcaAGCCAC aactacCTGA	2142
cctcacatGC cacaactAA cgaagatCCC tcgtctgCA actaAGTCCT agtgcAGTTA	2202
aatatatTT tttaatgcAC ttgaaatgtG agaatGAATG atgtgtcaca gacactgttG	2262
tccctgaga agggagtGAG taatgatttG agggccCTCA tagtatatCT tccttttAG	2322

ga ccc aga gac agg gac tgg ctt ggt gtc tca agg cag ctc aga att	2369
Gly Pro Arg Asp Arg Asp Trp Leu Gly Val Ser Arg Gln Ile Arg Ile	
<i>256 Insert</i> 30 35 40	

aaa gca tgg aac aga cag ctg tat cca gag tgg aca gaa agc cag ggg	2417
Lys Ala Trp Asn Arg Gln Leu Tyr Pro Glu Trp Thr Glu Ser Gln Gly	
45 50 55	

cct gac tgc tgg aga g gtaggaactt ggcaatttcc agggaggata tgggtggaaat	2473
Pro Asp Cys Trp Arg	
60	

gggtggggag gggAACGGGG ttgaaatgtac ttaggaAGAT agggAAGGAA aaggcataca	2533
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10/365, 646
from Seq 5 8

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							Asp	
caa tac tgg	caa gtt ctg	ggg ggc	cca gtg	tct gga	ctg agc	atc ggg		4361
Gln Tyr Trp	Gln Val	Leu Gly	Gly Pro	Val Ser	Gly Leu	Ser Ile	Gly	
160	165				170			
aca gac aag	gca atg ctg	ggc aca tat	aac atg	gaa gtg	act gtc	tac		4409
Thr Asp Lys	Ala Met	Leu Gly	Thr Tyr	Asn Met	Glu Val	Thr Val	Tyr	
175	180				185			
cac cgc cgg	ggg tcc cag	agc tat	gtg ccc	ctc gct	cac tcc	agt tca		4457
His Arg Arg	Gly Ser Gln	Ser Tyr Val	Pro Leu	Ala His	Ser Ser	Ser		
190	195			200				
gcc ttc acc att	act g	gtaaggactg	aggaggggac	aaggccagtt	gcagggcagg			4513
Ala Phe Thr	Ile Thr							
205								
agaaggtggg	gaggctggc	tggacaggaa	agggaaaaga	ggaaatggtg	tgtaacctta			4573
caggggcaga	accaggaaga	tgtggcaga	ggatgtggg	gcttggagcc	cgtgaaggc			4633
caggcagctt	gggttggttg	aaaaatatgg	ctgtgaaaga	agaagctgac	agaaagaaga			4693
acttatggtt	ctcaacttct	ctgactccaa	tcccag	ac cag	gtg ccc ttc	tct		4746
				Asp Gln	Val Pro	Phe Ser		
				210 ← Insert		215		
gtg agt gtg	tct cag	ctg cag	gcc ttg	gat gga	agg aac	aag cgc	ttc	4794
Val Ser Val	Ser Gln	Leu Gln	Ala Leu	Asp Gly	Arg Asn	Lys Arg	Phe	
220	225				230			
ctg aga aag	cag cct	ctg acc	ttt gcc	ctc cag	ctc cat	gat ccc	agt	4842
Leu Arg Lys	Gln Pro	Leu Thr	Phe Ala	Leu Gln	Leu His	Asp Pro	Ser	
235	240				245			
ggc tat ttg	gct ggg	gct gac	ctt tcc	acc tac	tgg gac	ttt ggt	gac	4890
Gly Tyr	Leu Ala	Gly Ala	Asp Leu	Ser Tyr	Thr Trp	Asp Phe	Gly Asp	
250	255				260			
agt aca ggg	acc ctg	atc tct	cgg gca	ctc acg	gtc act	cac act	tac	4938
Ser Thr Gly	Thr Leu Ile	Ser Arg	Ala Leu	Thr Val	Thr His	Thr Tyr		
265	270				275			
cta gag tct	ggc cca	gtc act	gca cag	gtg gtg	ctg cag	gct gcc	att	4986
Leu Glu Ser	Gly Pro	Val Thr	Ala Gln	Val Val	Leu Gln	Ala Ala	Ile	
280	285			290		295		
cct ctc acc	tcc tgt	ggc tcc	tct cca	gtt cca	ggc act	aca gat	agg	5034
Pro Leu Thr	Ser Cys	Gly Ser	Ser Pro	Val Pro	Gly Thr	Thr Asp	Arg	
300	305				310			
cat gtg aca	act gca	gag gct	cct gga	acc aca	gct ggc	caa gtg	cct	5082
His Val Thr	Thr Ala	Glu Ala	Pro Gly	Thr Thr	Ala Gly	Gln Val	Pro	
315	320				325			
act aca gaa	gtc atg	ggc acc	aca cct	ggc cag	gtg cca	act gca	gag	5130

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/565,646

DATE: 01/30/2006
TIME: 16:00:02

Input Set : A:\PTO.SS.txt
Output Set: N:\CRF4\01302006\J565646.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
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L:55 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:48
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L:324 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
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L:699 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 3
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L:1373 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 5
L:1605 M:254 E: No. of Bases conflict, this line has no nucleotides.